Application No.: 09/876235 Docket No.: COTH-P07-701

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

1-62. (Cancelled).

63. (Currently Amended) A molecule comprising a nucleic acid portion and a protein portion covalently bound to said nucleic acid portion through a peptide acceptor, wherein said protein portion is encoded by said nucleic acid portion and said peptide acceptor is not a tRNA and is a molecule capable of being added to the C-terminus of a growing protein chain by the catalytic activity of the ribosomal peptidyl transferase function.

64. (Previously Presented) The molecule of claim 63, wherein said protein portion comprises two or more amino acids joined by one or more peptide bonds.

65. (Previously Presented) A method for constructing the molecule as defined in claim 63, said method comprising (a) preparing a DNA containing a protein coding sequence; (b) transcribing the DNA into RNA; (c) covalently bonding to the 3' end of the protein coding sequence a peptide acceptor; and (d) translating the RNA in a cell-free protein synthesis system, thereby constructing the molecule of claim 63.

66. (Previously Presented) The method of claim 65, wherein step (a) comprises synthesizing a DNA primer and a DNA template, and amplifying said DNA template using said DNA primer via polymerase chain reaction.

67. (Previously Presented) The method of claim 65, wherein said cell-free protein synthesis system in step (d) is a wheat germ system or a reticulocyte system.

68. (Previously Presented) A method for *in vitro* selection and evolution, wherein said method comprises the steps of:

(a) constructing a first plurality of molecules, wherein each molecule is a molecule according to claim 63;

(b) selecting one or more molecules from said plurality, thereby obtaining one or more first selected molecules;

(c) using the nucleic acid portion of the one or more first selected molecules to mutagenically construct a second plurality of molecules, wherein each molecule is a molecule according to claim 63.

69. (Previously Presented) The method according to claim 68, further comprising the additional step of selecting one or more molecules from said second plurality, thereby obtaining one or more second selected molecules, wherein the nucleic acid and protein portions of said one or more second selected molecules differ from the nucleic acid and protein portions of said one or more first selected molecule.

70. (Previously Presented) The method according to claim 68, wherein said selecting steps comprises contacting said first plurality of molecules with a target molecule or immobilized selection motif.

71. (Previously Presented) The method according to claim 69, wherein said selecting steps are carried out by contacting said first and second plurality of molecules with a target molecule or immobilized selection motif.

72. (Previously Presented) The method according to any of claims 68-71, wherein step (c) comprises amplification via mutagenic PCR.

73. (Previously Presented) A method for assaying protein/protein or protein/nucleic acid interaction, which comprises the steps of (a) constructing a molecule according to claim 63, and (b) determining whether said molecule interacts with another protein or nucleic acid, thereby assaying protein/protein or protein/nucleic acid interaction.

74. (Previously Presented) The method of claim 73, wherein step (b) is carried out by combining the molecule according to claim 63 with an antibody, and determining whether said antibody binds to the protein portion of said molecule.

75. (Previously Presented) The method according to any of claims 73 and 74, wherein said step (b) comprises an immunoprecipitation reaction.

76. (Previously Presented) The method according to claim 75, wherein said immunoprecipitation reaction is carried out with a c-myc antibody.

77. (Previously Presented) The molecule according to claim 63, wherein the peptide acceptor is puromycin.

78. (Cancelled)

79. (Cancelled)